

SEQUENCE LISTING

<110> Ono Pharmaceutical Co., Ltd.

<120> Novel Polypeptides, DNAs encoding the polypeptides, and utility of the Polypeptides

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<141> 1999-08-27

<150> JP 9-43143

<151> 1997-02-27

<150> PCT/JP98/00799

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<170> PatentIn version 3.0

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<223> Origin: human bone marrow stromal cell line HAS303

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<223> Origin: human bone marrow stromal cell line HAS303

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<223> Origin: human bone marrow stromal cell line HAS303

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104

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152

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296

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344

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392

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95 100 105

440

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110 115 120

488

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536

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Phe Met Glu Lys Lys Pro Ser Trp Ser Leu Arg Ser Gln Asp Ile Gln			
175	180	185	
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Tyr Asn Gly Ser Glu Leu Ser Cys Leu Asp Arg Pro Gln Leu His Glu			
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Leu Glu Ser Ser Thr Ser Leu Asp Ser Asn Ser Ser Gln Asp Leu Val			
320	325	330	
ggt ggg gct gtt cca gtc cag tct cat tct gaa aac ttt aca gca gct			1160
Gly Gly Ala Val Pro Val Gln Ser His Ser Glu Asn Phe Thr Ala Ala			
335	340	345	
act gat tta tct aga tat aac aac aca ctg gta gaa tca gca tca act			1208
Thr Asp Leu Ser Arg Tyr Asn Asn Thr Leu Val Glu Ser Ala Ser Thr			

350

355

360

cag gat gca cta act atg aga agc cag cta gat cag gag agt ggc gct	1256														
Gln Asp Ala Leu Thr Met Arg Ser Gln Leu Asp Gln Glu Ser Gly Ala															
365	370	375		atc atc cac cca gcc act cag acg tcc ctc cag gta agg cag cga ctg	1304	Ile Ile His Pro Ala Thr Gln Thr Ser Leu Gln Val Arg Gln Arg Leu		380	385	390	395	ggt tcc ctg tgaacacagc actgacttac agtagatcag aactctgttc	1353	Gly Ser Leu	
375															
atc atc cac cca gcc act cag acg tcc ctc cag gta agg cag cga ctg	1304														
Ile Ile His Pro Ala Thr Gln Thr Ser Leu Gln Val Arg Gln Arg Leu															
380	385	390	395	ggt tcc ctg tgaacacagc actgacttac agtagatcag aactctgttc	1353	Gly Ser Leu									
390	395														
ggt tcc ctg tgaacacagc actgacttac agtagatcag aactctgttc	1353														
Gly Ser Leu															

ccagcataag atttggggga acctgatgag tttttttt gcatcttaa taatttcttg	1413
tatgtttag agtatgtttt aaaataaatt tcaagtattt tttttaaaaaa ctaaaaaaaaaa	1473
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Leu Val Leu Leu Gly Tyr Leu Ser Cys Lys Val Thr Cys Glu Thr Gly
 -5 -1 1 5

Asp Cys Arg Gln Gln Glu Phe Arg Asp Arg Ser Gly Asn Cys Val Pro
 10 15 20

Cys Asn Gln Cys Gly Pro Gly Met Glu Leu Ser Lys Glu Cys Gly Phe
 25 30 35

Gly Tyr Gly Glu Asp Ala Gln Cys Val Thr Cys Arg Leu His Arg Phe
 40 45 50 55

Lys Glu Asp Trp Gly Phe Gln Lys Cys Lys Pro Cys Leu Asp Cys Ala
 60 65 70

Val Val Asn Arg Phe Gln Lys Ala Asn Cys Ser Ala Thr Ser Asp Ala

75

80

85

Ile Cys Gly Asp Cys Leu Pro Gly Phe Tyr Arg Lys Thr Lys Leu Val
 90 95 100

Gly Phe Gln Asp Met Glu Cys Val Pro Cys Gly Asp Pro Pro Pro Pro
 105 110 115

Tyr Glu Pro His Cys Ala Ser Lys Val Asn Leu Val Lys Ile Ala Ser
 120 125 130 135

Thr Ala Ser Ser Pro Arg Asp Thr Ala Leu Ala Ala Val Ile Cys Ser
 140 145 150

Ala Leu Ala Thr Val Leu Leu Ala Leu Leu Ile Leu Cys Val Ile Tyr
 155 160 165

Cys Lys Arg Gln Phe Met Glu Lys Lys Pro Ser Trp Ser Leu Arg Ser
 170 175 180

Gln Asp Ile Gln Tyr Asn Gly Ser Glu Leu Ser Cys Leu Asp Arg Pro
 185 190 195

Gln Leu His Glu Tyr Ala His Arg Ala Cys Cys Gln Cys Arg Arg Asp
 200 205 210 215

Ser Val Gln Thr Cys Gly Pro Val Arg Leu Leu Pro Ser Met Cys Cys
 220 225 230

Glu Glu Ala Cys Ser Pro Asn Pro Ala Thr Leu Gly Cys Gly Val His
 235 240 245

Ser Ala Ala Ser Leu Gln Ala Arg Asn Ala Gly Pro Ala Gly Glu Met
 250 255 260

Val Pro Thr Phe Phe Gly Ser Leu Thr Gln Ser Ile Cys Gly Glu Phe
 265 270 275

Ser Asp Ala Trp Pro Leu Met Gln Asn Pro Met Gly Gly Asp Asn Ile
 280 285 290 295

Ser Phe Cys Asp Ser Tyr Pro Glu Leu Thr Gly Glu Asp Ile His Ser
 300 305 310

Leu Asn Pro Glu Leu Glu Ser Ser Thr Ser Leu Asp Ser Asn Ser Ser
315 320 325

Gln Asp Leu Val Gly Gly Ala Val Pro Val Gln Ser His Ser Glu Asn
330 335 340

Phe Thr Ala Ala Thr Asp Leu Ser Arg Tyr Asn Asn Thr Leu Val Glu
345 350 355

Ser Ala Ser Thr Gln Asp Ala Leu Thr Met Arg Ser Gln Leu Asp Gln
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380 385 390

Arg Gln Arg Leu Gly Ser Leu
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<212> DNA
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28